

1633

RAW SEQUENCE LISTING

DATE: 05/25/2000

PATENT APPLICATION: US/09/388,221A

TIME: 15:49:41

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Output Set : N:\CRF3\05252000\I388221A.raw

3 <110> APPLICANT: Reed, John C.
5 <120> TITLE OF INVENTION: Novel Card Proteins Involved in Cell Death Regulation
7 <130> FILE REFERENCE: P-LJ 3650
9 <140> CURRENT APPLICATION NUMBER: 09/388,221A
10 <141> CURRENT FILING DATE: 1999-09-01
12 <160> NUMBER OF SEQ ID NOS: 18
14 <170> SOFTWARE: PatentIn Ver. 2.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 4422
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (1)..(4422)
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27 Met Ala Gly Gly Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu
28 1 5 10 15
30 aag aag gag gag ctg aag gag ttc cag ctt ctg ctc gcc aat aaa gcg 96
31 Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala
32 20 25 30
34 cac tcc agg agc tct tgg ggt gag aca ccc gct cag cca gag aag acg 144
35 His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr
36 35 40 45
38 agt ggc atg gag gtg gcc tgg tac ctg gtg gct cag tat ggg gag cag 192
39 Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln
40 50 55 60
42 cgg gcc tgg gac cta gcc ctc cat acc tgg gag cag atg ggg ctg agg 240
43 Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg
44 65 70 75 80
46 tca ctg tgc gcc caa gcc cag gaa ggg gca ggc cac tct ccc tca ttc 288
47 Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe
48 85 90 95
50 ccc tac agc cca agt gaa ccc cac ctg ggg tct ccc agc caa ccc acc 336
51 Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr
52 100 105 110
54 tcc acc gca gtg cta atg ccc tgg atc cat gaa ttg ccg gcg ggg tgc 384
55 Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys
56 115 120 125
58 acc cag ggc tca gag aga agg gtt ttg aga cag ctg cct gac aca tct 432
59 Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser
60 130 135 140
62 gga cgc cgc tgg aga gaa atc tct gcc tca ctc ctc tac caa gct ctt 480
63 Gly Arg Arg Trp Arg Glu Ile Ser Ala Ser Leu Leu Tyr Gln Ala Leu
64 145 150 155 160
66 cca agc tcc cca gac cat gag tct cca agc cag gag tca ccc aac gcc 528
67 Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala

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70 ccc aca tcc aca gca gtg ctg ggg agc tgg gga tcc cca cct cag ccc 576
71 Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro
72          180          185          190
74 agc cta gca ccc aga gag cag gag gct cct ggg acc caa tgg cct ctg 624
75 Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu
76          195          200          205
78 gat gaa acg tca gga att tac tac aca gaa atc aga gaa aga gag aga 672
79 Asp Glu Thr Ser Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg
80          210          215          220
82 gag aaa tca gag aaa ggc agg ccc cca tgg gca gcg gtg gta gga acg 720
83 Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr
84 225          230          235          240
86 ccc cca cag gcg cac acc agc cta cag ccc cac cac cca tgg gag 768
87 Pro Pro Gln Ala His Thr Ser Leu Gln Pro His His His Pro Trp Glu
88          245          250          255
90 cct tct gtg aga gag agc ctc tgt tcc aca tgg ccc tgg aaa aat gag 816
91 Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu
92          260          265          270
94 gat ttt aac caa aaa ttc aca cag ctg cta ctt cta caa aga cct cac 864
95 Asp Phe Asn Gln Lys Phe Thr Gln Leu Leu Leu Leu Gln Arg Pro His
96          275          280          285
98 ccc aga agc caa gat ccc ctg gtc aag aga agc tgg cct gat tat gtg 912
99 Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val
100          290          295          300
102 gag gag aat cga gga cat tta att gag atc aga gac tta ttt ggc cca 960
103 Glu Glu Asn Arg Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro
104 305          310          315          320
106 ggc ctg gat acc caa gaa cct cgc ata gtc ata ctg cag ggg gct gct 1008
107 Gly Leu Asp Thr Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala
108          325          330          335
110 gga att ggg aag tca aca ctg gcc agg cag gtg aag gaa gcc tgg ggg 1056
111 Gly Ile Gly Lys Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly
112          340          345          350
114 aga ggc cag ctg tat ggg gac cgc ttc cag cat gtc ttc tac ttc agc 1104
115 Arg Gly Gln Leu Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser
116          355          360          365
118 tgc aga gag ctg gcc cag tcc aag gtg gtg agt ctc gct gag ctc atc 1152
119 Cys Arg Glu Leu Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile
120          370          375          380
122 gga aaa gat ggg aca gcc act ccg gct ccc att aga cag atc ctg tct 1200
123 Gly Lys Asp Gly Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser
124 385          390          395          400
126 agg cca gag cgg ctg ctc ttc atc ctc gat ggt gta gat gag cca gga 1248
127 Arg Pro Glu Arg Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly
128          405          410          415
130 tgg gtc ttg cag gag ccg agt tct gag ctc tgt ctg cac tgg agc cag 1296
131 Trp Val Leu Gln Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln
132          420          425          430

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134 cca cag ccg gcg gat gca ctg ctg ggc agt ttg ctg ggg aaa act ata 1344
135 Pro Gln Pro Ala Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile
136      435      440      445
138 ctt ccc gag gca tcc ttc ctg atc acg gct cgg acc aca gct ctg cag 1392
139 Leu Pro Glu Ala Ser Phe Leu Ile Thr Ala Arg Thr Thr Ala Leu Gln
140      450      455      460
142 aac ctc att cct tct ttg gag gca cgt tgg gta gag gtc ctg ggg 1440
143 Asn Leu Ile Pro Ser Leu Glu Gln Ala Arg Trp Val Glu Val Leu Gly
144 465      470      475      480
146 ttc tct gag tcc agc agg aag gaa tat ttc tac aga tat ttc aca gat 1488
147 Phe Ser Glu Ser Ser Arg Lys Glu Tyr Phe Tyr Arg Tyr Phe Thr Asp
148      485      490      495
150 gaa agg caa gca att aga gcc ttt agg ttg gtc aaa tca aac aaa gag 1536
151 Glu Arg Gln Ala Ile Arg Ala Phe Arg Leu Val Lys Ser Asn Lys Glu
152      500      505      510
154 ctc tgg gcc ctg tgt ctt gtg ccc tgg gtg tcc tgg ctg gcc tgc act 1584
155 Leu Trp Ala Leu Cys Leu Val Pro Trp Val Ser Trp Leu Ala Cys Thr
156      515      520      525
158 tgc ctg atg cag cag atg aag cgg aag gaa aaa ctc aca ctg act tcc 1632
159 Cys Leu Met Gln Gln Met Lys Arg Lys Glu Lys Leu Thr Leu Thr Ser
160      530      535      540
162 aag acc acc aca acc ctc tgt cta cat tac ctt gcc cag gct ctc caa 1680
163 Lys Thr Thr Thr Thr Leu Cys Leu His Tyr Leu Ala Gln Ala Leu Gln
164 545      550      555      560
166 gct cag cca ttg gga ccc cag ctc aga gac ctc tgc tct ctg gct gct 1728
167 Ala Gln Pro Leu Gly Pro Gln Leu Arg Asp Leu Cys Ser Leu Ala Ala
168      565      570      575
170 gag ggc atc tgg caa aaa aag acc ctt ttc agt cca gat gac ctc agg 1776
171 Glu Gly Ile Trp Gln Lys Lys Thr Leu Phe Ser Pro Asp Asp Leu Arg
172      580      585      590
174 aag cat ggg tta gat ggg gcc atc atc tcc acc ttc ttg aag atg ggt 1824
175 Lys His Gly Leu Asp Gly Ala Ile Ile Ser Thr Phe Leu Lys Met Gly
176      595      600      605
178 att ctt caa gag cac ccc atc cct ctg agc tac agc ttc att cac ctc 1872
179 Ile Leu Gln Glu His Pro Ile Pro Leu Ser Tyr Ser Phe Ile His Leu
180      610      615      620
182 tgt ttc caa gag ttc ttt gca gca atg tcc tat gtc ttg gag gat gag 1920
183 Cys Phe Gln Glu Phe Phe Ala Ala Met Ser Tyr Val Leu Glu Asp Glu
184 625      630      635      640
186 aag ggg aga ggt aaa cat tct aat tgc atc ata gat ttg gaa aag acg 1968
187 Lys Gly Arg Gly Lys His Ser Asn Cys Ile Ile Asp Leu Glu Lys Thr
188      645      650      655
190 cta gaa gca tat gga ata cat ggc ctg ttt ggg gca tca acc aca cgt 2016
191 Leu Glu Ala Tyr Gly Ile His Gly Leu Phe Gly Ala Ser Thr Thr Arg
192      660      665      670
194 ttc cta ttg ggc ctg tta agt gat gag ggg gag aga gag atg gag aac 2064
195 Phe Leu Leu Gly Leu Leu Ser Asp Glu Gly Glu Arg Glu Met Glu Asn
196      675      680      685
198 atc ttt cac tgc cgg ctg tct cag ggg agg aac ctg atg cag tgg gtc 2112

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200		690					695					700					
202	ccg	tcc	ctg	cag	ctg	ctg	ctg	cag	cca	cac	tct	ctg	gag	tcc	ctc	cac	2160
203	Pro	Ser	Leu	Gln	Leu	Leu	Gln	Pro	His	Ser	Leu	Glu	Ser	Leu	His		
204	705					710				715					720		
206	tgc	ttg	tac	gag	act	cgg	aac	aaa	acg	ttc	ctg	aca	caa	gtg	atg	gcc	2208
207	Cys	Leu	Tyr	Glu	Thr	Arg	Asn	Lys	Thr	Phe	Leu	Thr	Gln	Val	Met	Ala	
208					725					730					735		
210	cat	ttc	gaa	gaa	atg	ggc	atg	tgt	gta	gaa	aca	gac	atg	gag	ctc	tta	2256
211	His	Phe	Glu	Glu	Met	Gly	Met	Cys	Val	Glu	Thr	Asp	Met	Glu	Leu	Leu	
212				740					745					750			
214	gtg	tgc	act	ttc	tgc	att	aaa	ttc	agc	cgc	cac	gtg	aag	aag	ctt	cag	2304
215	Val	Cys	Thr	Phe	Cys	Ile	Lys	Phe	Ser	Arg	His	Val	Lys	Lys	Leu	Gln	
216			755					760					765				
218	ctg	att	gag	ggc	agg	cag	cac	aga	tca	aca	tgg	agc	ccc	acc	atg	gta	2352
219	Leu	Ile	Glu	Gly	Arg	Gln	His	Arg	Ser	Thr	Trp	Ser	Pro	Thr	Met	Val	
220		770					775						780				
222	gtc	ctg	ttc	agg	tgg	gtc	cca	gtc	aca	gat	gcc	tat	tgg	cag	att	ctc	2400
223	Val	Leu	Phe	Arg	Trp	Val	Pro	Val	Thr	Asp	Ala	Tyr	Trp	Gln	Ile	Leu	
224	785					790					795					800	
226	ttc	tcc	gtc	ctc	aag	gtc	acc	aga	aac	ctg	aag	gag	ctg	gac	cta	agt	2448
227	Phe	Ser	Val	Leu	Lys	Val	Thr	Arg	Asn	Leu	Lys	Glu	Leu	Asp	Leu	Ser	
228					805					810					815		
230	gga	aac	tcg	ctg	agc	cac	tct	gca	gtg	aag	agt	ctt	tgt	aag	acc	ctg	2496
231	Gly	Asn	Ser	Leu	Ser	His	Ser	Ala	Val	Lys	Ser	Leu	Cys	Lys	Thr	Leu	
232				820					825					830			
234	aga	cgc	cct	cgc	tgc	ctc	ctg	gag	acc	ctg	cgg	ttg	gct	ggc	tgt	ggc	2544
235	Arg	Arg	Pro	Arg	Cys	Leu	Leu	Glu	Thr	Leu	Arg	Leu	Ala	Gly	Cys	Gly	
236			835					840					845				
238	ctc	aca	gct	gag	gac	tgc	aag	gac	ctt	gcc	ttt	ggg	ctg	aga	gcc	aac	2592
239	Leu	Thr	Ala	Glu	Asp	Cys	Lys	Asp	Leu	Ala	Phe	Gly	Leu	Arg	Ala	Asn	
240		850					855					860					
242	cag	acc	ctg	acc	gag	ctg	gac	ctg	agc	ttc	aat	gtg	ctc	acg	gat	gct	2640
243	Gln	Thr	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Phe	Asn	Val	Leu	Thr	Asp	Ala	
244	865					870					875				880		
246	gga	gcc	aaa	cac	ctt	tgc	cag	aga	ctg	aga	cag	ccg	agc	tgc	aag	cta	2688
247	Gly	Ala	Lys	His	Leu	Cys	Gln	Arg	Leu	Arg	Gln	Pro	Ser	Cys	Lys	Leu	
248					885					890					895		
250	cag	cga	ctg	cag	ctg	gtc	agc	tgt	ggc	ctc	acg	tct	gac	tgc	tgc	cag	2736
251	Gln	Arg	Leu	Gln	Leu	Val	Ser	Cys	Gly	Leu	Thr	Ser	Asp	Cys	Cys	Gln	
252			900						905					910			
254	gac	ctg	gcc	tct	gtg	ctt	agt	gcc	agc	ccc	agc	ctg	aag	gag	cta	gac	2784
255	Asp	Leu	Ala	Ser	Val	Leu	Ser	Ala	Ser	Pro	Ser	Leu	Lys	Glu	Leu	Asp	
256			915					920					925				
258	ctg	cag	cag	aac	aac	ctg	gat	gac	gtt	ggc	gtg	cga	ctg	ctc	tgt	gag	2832
259	Leu	Gln	Gln	Asn	Asn	Leu	Asp	Asp	Val	Gly	Val	Arg	Leu	Leu	Cys	Glu	
260		930					935						940				
262	ggg	ctc	agg	cat	cct	gcc	tgc	aaa	ctc	ata	cgc	ctg	ggg	ctg	gac	cag	2880
263	Gly	Leu	Arg	His	Pro	Ala	Cys	Lys	Leu	Ile	Arg	Leu	Gly	Leu	Asp	Gln	

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266 aca act ctg agt gat gag atg agg cag gaa ctg agg gcc ctg gag cag 2928
267 Thr Thr Leu Ser Asp Glu Met Arg Gln Glu Leu Arg Ala Leu Glu Gln
268          965          970          975
270 gag aaa cct cag ctg ctc atc ttc agc aga cgg aaa cca agt gtg atg 2976
271 Glu Lys Pro Gln Leu Leu Ile Phe Ser Arg Arg Lys Pro Ser Val Met
272          980          985          990
274 acc cct act gag ggc ctg gat acg gga gag atg agt aat agc aca tcc 3024
275 Thr Pro Thr Glu Gly Leu Asp Thr Gly Glu Met Ser Asn Ser Thr Ser
276          995          1000          1005
278 tca ctc aag cgg cag aga ctc gga tca gag agg gcg gct tcc cat gtt 3072
279 Ser Leu Lys Arg Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser His Val
280          1010          1015          1020
282 gct cag gct aat ctc aaa ctc ctg gac gtg agc aag atc ttc cca att 3120
283 Ala Gln Ala Asn Leu Lys Leu Leu Asp Val Ser Lys Ile Phe Pro Ile
284          1025          1030          1035          1040
286 gct gag att gca gag gaa agc tcc cca gag gta gta ccg gtg gaa ctc 3168
287 Ala Glu Ile Ala Glu Glu Ser Ser Pro Glu Val Val Pro Val Glu Leu
288          1045          1050          1055
290 ttg tgc gtg cct tct cct gcc tct caa ggg gac ctg cat acg aag cct 3216
291 Leu Cys Val Pro Ser Pro Ala Ser Gln Gly Asp Leu His Thr Lys Pro
292          1060          1065          1070
294 ttg ggg act gag gat gac ttc tgg ggc ccc acg ggg cct gtg gct act 3264
295 Leu Gly Thr Asp Asp Phe Trp Gly Pro Thr Gly Pro Val Ala Thr
296          1075          1080          1085
298 gag gta gtt gac aaa gaa aag aac ttg tac cga gtt cac ttc cct gta 3312
299 Glu Val Val Asp Lys Glu Lys Asn Leu Tyr Arg Val His Phe Pro Val
300          1090          1095          1100
302 gct ggc tcc tac cgc tgg ccc aac acg ggt ctc tgc ttt gtg atg aga 3360
303 Ala Gly Ser Tyr Arg Trp Pro Asn Thr Gly Leu Cys Phe Val Met Arg
304          1105          1110          1115          1120
306 gaa gcg gtg acc gtt gag att gaa ttc tgt gtg tgg gac cag ttc ctg 3408
307 Glu Ala Val Thr Val Glu Ile Glu Phe Cys Val Trp Asp Gln Phe Leu
308          1125          1130          1135
310 ggt gag atc aac cca cag cac agc tgg atg gtg gca ggg cct ctg ctg 3456
311 Gly Glu Ile Asn Pro Gln His Ser Trp Met Val Ala Gly Pro Leu Leu
312          1140          1145          1150
314 gac atc aag gct gag cct gga gct gtg gaa gct gtg cac ctc cct cac 3504
315 Asp Ile Lys Ala Glu Pro Gly Ala Val Glu Ala Val His Leu Pro His
316          1155          1160          1165
318 ttt gtg gct ctc caa ggg ggc cat gtg gac aca tcc ctg ttc caa atg 3552
319 Phe Val Ala Leu Gln Gly Gly His Val Asp Thr Ser Leu Phe Gln Met
320          1170          1175          1180
322 gcc cac ttt aaa gag gag ggg atg ctc ctg gag aag cca gcc agg gtg 3600
323 Ala His Phe Lys Glu Glu Gly Met Leu Leu Glu Lys Pro Ala Arg Val
324          1185          1190          1195          1200
326 gag ctg cat cac ata gtt ctg gaa aac ccc agc ttc tcc ccc ttg gga 3648
327 Glu Leu His His Ile Val Leu Glu Asn Pro Ser Phe Ser Pro Leu Gly
328          1205          1210          1215

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VERIFICATION SUMMARY

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TIME: 15:49:42

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